

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/422,999B  
Source: IFW/6  
Date Processed by STIC: 6/14/05

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IFW16

## RAW SEQUENCE LISTING

DATE: 06/14/2005

PATENT APPLICATION: US/09/422,999B

TIME: 13:29:06

Input Set : A:\MIT-103.ST25.txt

Output Set: N:\CRF4\06132005\I422999B.raw

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3 <110> APPLICANT: Kawasaki, Hiroaki
4   Graybiel, Ann
5   Housman, David
7 <120> TITLE OF INVENTION: Genes Integrating Signal Transduction Pathways
9 <130> FILE REFERENCE: MIT-103
11 <140> CURRENT APPLICATION NUMBER: US 09/422,999B
12 <141> CURRENT FILING DATE: 1999-10-22
14 <150> PRIOR APPLICATION NUMBER: US 60/105,507
15 <151> PRIOR FILING DATE: 1998-10-23
17 <150> PRIOR APPLICATION NUMBER: US 60/108,685
18 <151> PRIOR FILING DATE: 1998-11-16
20 <160> NUMBER OF SEQ ID NOS: 67
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2250
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (166)..(1989)
34 <400> SEQUENCE: 1
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37 cgggtttgca ttctgaagta aaggacttgg gacaggggta cgaatcgagc actgtggggag      120
39 gctctgagag tgtaacttgg gtctagccca ctggcaccgg cagcc atg gcg agc act      177
40                                     Met Ala Ser Thr
41                                     1
43 ctg gac ctg gac aag ggt tgc acc gtg gag gag ctg ctc cgt ggc tgt      225
44 Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys
45 5                               10                               15                               20
47 atc gaa gcc ttt gat gac tct gga aag gtg cga gat cca cag cta gtg      273
48 Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val
49                               25                               30                               35
51 cgc atg ttt ctc atg atg cac ccc tgg tac ata cct tcc tct cag ctg      321
52 Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu
53                               40                               45                               50
55 gct tcg aaa ctg ctc cac ttc tat cag caa tcc cgg aag gac aac tcc      369
56 Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg Lys Asp Asn Ser
57                               55                               60                               65
59 aat tcc cta cag gtg aaa acc tgt cac ctg gtc agg tac tgg gtc tca      417
60 Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg Tyr Trp Val Ser
61                               70                               75                               80
63 gcc ttc cca gca gag ttc gac ttg aac cca gag ctg gct gaa ccg atc      465
64 Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Pro Ile

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65	85	90	95	100	
67	aag gag ctg aag gct ctg tta gac caa gaa gga aac cgc agg cac agc	513			
68	Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser				
69	105 110 115				
71	agc ctc atc gac atc gag agt gtc ccc acc tac aag tgg aag cgg cag	561			
72	Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln				
73	120 125 130				
75	gtg acc cag cgg aac cct gtg gaa cag aaa aag cgc aag atg tcc ctg	609			
76	Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg Lys Met Ser Leu				
77	135 140 145				
79	ttg ttt gat cac ttg gag cct atg gaa ctg gca gaa cat ctc acc tac	657			
80	Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr				
81	150 155 160				
83	ttg gag tat cgg tcc ttc tgc aag atc ctg ttc cag gac tat cac agc	705			
84	Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser				
85	165 170 175 180				
87	ttt gtg act cat ggc tgc act gta gac aat ccg gtc ctg gag cga ttc	753			
88	Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe				
89	185 190 195				
91	atc tcc ctc ttc aac agt gtc tct cag tgg gtc caa ctc atg atc ctc	801			
92	Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu				
93	200 205 210				
95	agc aag ccc aca gcc acg cag cgg gcg ctg gtc atc aca cat ttc gtg	849			
96	Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile Thr His Phe Val				
97	215 220 225				
99	cat gtg gca gag aag ctg ctg cag ctg cag aac ttc aac acg ttg atg	897			
100	His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met				
101	230 235 240				
103	gcc gtc gtg gga ggc ctg agc cac agc tcc atc tca cgc ctc aag gag	945			
104	Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu				
105	245 250 255 260				
107	acc cac agc cat gtc agc cct gac acc atc aag ctc tgg gaa ggt ctg	993			
108	Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu Trp Glu Gly Leu				
109	265 270 275				
111	aca gaa cta gtg aca gct act ggc aac tac agc aac tac cgg cga agg	1041			
112	Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn Tyr Arg Arg Arg				
113	280 285 290				
115	ctg gcg gcc tgc gtg ggc ttc cgc ttt cct atc ctg ggt gtg cac ctc	1089			
116	Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu				
117	295 300 305				
119	aag gat cta gtg gct ctg cag ctg gct ctg cct gac tgg ctg gac cca	1137			
120	Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp Trp Leu Asp Pro				
121	310 315 320				
123	ggt cgg acc cgg ctc aat gga gcc aag atg agg cag ctt ttc agc att	1185			
124	Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln Leu Phe Ser Ile				
125	325 330 335 340				
127	ctg gag gag ttg gct atg gtg acc agt ctt cga cca cca gtg caa gcc	1233			
128	Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala				
129	345 350 355				

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131	aac	ccc	gac	ctg	ctg	agt	ctg	ctc	acg	gtg	tcc	ctg	gac	cag	tat	cag	1281
132	Asn	Pro	Asp	Leu	Leu	Ser	Leu	Leu	Thr	Val	Ser	Leu	Asp	Gln	Tyr	Gln	
133				360					365					370			
135	acg	gag	gat	gag	ctg	tat	cag	ctc	tct	ctg	cag	cga	gag	cca	cgt	tcc	1329
136	Thr	Glu	Asp	Glu	Leu	Tyr	Gln	Leu	Ser	Leu	Gln	Arg	Glu	Pro	Arg	Ser	
137				375				380					385				
139	aag	tca	tcg	ccc	acc	agc	ccc	acc	agc	tgc	acc	ccg	cct	ccc	cgg	ccg	1377
140	Lys	Ser	Ser	Pro	Thr	Ser	Pro	Thr	Ser	Cys	Thr	Pro	Pro	Pro	Arg	Pro	
141				390				395					400				
143	cct	gtg	ctg	gaa	gag	tgg	acc	tca	gtt	gcc	aag	cct	aag	ctg	gac	caa	1425
144	Pro	Val	Leu	Glu	Glu	Trp	Thr	Ser	Val	Ala	Lys	Pro	Lys	Leu	Asp	Gln	
145	405					410					415					420	
147	gcc	ttg	gtg	gcc	gag	cac	att	gag	aag	atg	gtg	gag	tct	gtg	ttc	cgg	1473
148	Ala	Leu	Val	Ala	Glu	His	Ile	Glu	Lys	Met	Val	Glu	Ser	Val	Phe	Arg	
149					425					430					435		
151	aac	ttt	gac	gtt	gat	ggg	gac	ggg	cac	atc	tcc	cag	gag	gag	ttc	cag	1521
152	Asn	Phe	Asp	Val	Asp	Gly	Asp	Gly	His	Ile	Ser	Gln	Glu	Glu	Phe	Gln	
153				440				445						450			
155	atc	atc	cgg	ggc	aac	ttc	cct	tat	ctc	agc	gcc	ttt	ggg	gac	ttg	gac	1569
156	Ile	Ile	Arg	Gly	Asn	Phe	Pro	Tyr	Leu	Ser	Ala	Phe	Gly	Asp	Leu	Asp	
157				455				460					465				
159	cag	aac	cag	gat	ggc	tgc	atc	agc	cgg	gag	gag	atg	att	tcc	tac	ttc	1617
160	Gln	Asn	Gln	Asp	Gly	Cys	Ile	Ser	Arg	Glu	Glu	Met	Ile	Ser	Tyr	Phe	
161				470				475					480				
163	ctg	cgc	tcc	agc	tcc	gtg	ctg	gga	ggc	cgc	atg	ggc	ttc	gta	cac	aac	1665
164	Leu	Arg	Ser	Ser	Ser	Val	Leu	Gly	Gly	Arg	Met	Gly	Phe	Val	His	Asn	
165	485					490					495					500	
167	ttc	cag	gag	agt	aac	tcg	cta	agg	ccg	gtc	gcc	tgc	cga	cac	tgc	aaa	1713
168	Phe	Gln	Glu	Ser	Asn	Ser	Leu	Arg	Pro	Val	Ala	Cys	Arg	His	Cys	Lys	
169					505					510					515		
171	gct	ctg	atc	ctg	ggc	atc	tac	aag	cag	ggc	ctc	aaa	tgt	aga	gct	tgt	1761
172	Ala	Leu	Ile	Leu	Gly	Ile	Tyr	Lys	Gln	Gly	Leu	Lys	Cys	Arg	Ala	Cys	
173				520					525					530			
175	ggg	gtg	aac	tgc	cac	aag	cag	tgc	aaa	gac	cga	ctg	tca	gtg	gaa	tgt	1809
176	Gly	Val	Asn	Cys	His	Lys	Gln	Cys	Lys	Asp	Arg	Leu	Ser	Val	Glu	Cys	
177				535				540					545				
179	cgc	cgc	cgc	gcc	cag	agt	gtg	agc	ctg	gag	ggc	tct	gca	ccc	tct	ccc	1857
180	Arg	Arg	Arg	Ala	Gln	Ser	Val	Ser	Leu	Glu	Gly	Ser	Ala	Pro	Ser	Pro	
181				550				555					560				
183	tca	ccc	aca	cat	acc	cac	cat	cgg	gcc	ttc	agc	ttc	tcc	ctg	cct	cgc	1905
184	Ser	Pro	Thr	His	Thr	His	His	Arg	Ala	Phe	Ser	Phe	Ser	Leu	Pro	Arg	
185	565					570					575					580	
187	cca	ggc	agg	cgc	agc	tct	cgg	cct	cca	gag	atc	cgt	gaa	gag	gag	gtg	1953
188	Pro	Gly	Arg	Arg	Ser	Ser	Arg	Pro	Pro	Glu	Ile	Arg	Glu	Glu	Glu	Val	
189					585					590					595		
191	cag	act	gtg	gaa	gat	ggg	gtg	ttc	gac	atc	cac	tta	taagacgctg				1999
192	Gln	Thr	Val	Glu	Asp	Gly	Val	Phe	Asp	Ile	His	Leu					
193				600						605							
195	tgactatcaa	ggactcattc	ctgccttggg	gaaaagactt	ggagcagagc	agggagccag											2059

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197 ggattctggg gcaggaggtt ggggctgaag gtgggggaag ttgaagggtg catgcactga 2119
199 aaaaaaggcc agggctggtg tccctaaggt tgtacagact tctgtgaata tttgtatttt 2179
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203 aaaaaaaaaa a 2250
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208 <212> TYPE: PRT
209 <213> ORGANISM: Mus musculus
211 <400> SEQUENCE: 2
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217 Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp
218 20 25 30
221 Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro
222 35 40 45
225 Ser Ser Gln Leu Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg
226 50 55 60
229 Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg
230 65 70 75 80
233 Tyr Trp Val Ser Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu
234 85 90 95
237 Ala Glu Pro Ile Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn
238 100 105 110
241 Arg Arg His Ser Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys
242 115 120 125
245 Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg
246 130 135 140
249 Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu
250 145 150 155 160
253 His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln
254 165 170 175
257 Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val
258 180 185 190
261 Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln
262 195 200 205
265 Leu Met Ile Leu Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile
266 210 215 220
269 Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe
270 225 230 235 240
273 Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser
274 245 250 255
277 Arg Leu Lys Glu Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu
278 260 265 270
281 Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn
282 275 280 285
285 Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu
286 290 295 300
289 Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp
290 305 310 315 320

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293 Trp Leu Asp Pro Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln
294           325           330           335
297 Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro
298           340           345           350
301 Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu
302           355           360           365
305 Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg
306           370           375           380
309 Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro
310 385           390           395           400
313 Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro
314           405           410           415
317 Lys Leu Asp Gln Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu
318           420           425           430
321 Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln
322           435           440           445
325 Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe
326           450           455           460
329 Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met
330 465           470           475           480
333 Ile Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly
334           485           490           495
337 Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys
338           500           505           510
341 Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys
342           515           520           525
345 Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu
346           530           535           540
349 Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser
350 545           550           555           560
353 Ala Pro Ser Pro Ser Pro Thr His Thr His His Arg Ala Phe Ser Phe
354           565           570           575
357 Ser Leu Pro Arg Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg
358           580           585           590
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362           595           600           605
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366 <211> LENGTH: 2236
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
371 <220> FEATURE:
372 <221> NAME/KEY: CDS
373 <222> LOCATION: (161)..(1987)
375 <400> SEQUENCE: 3
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380 ggagcgcagc ctgggccccag cccaccccgcc gccggcgccc atg gca ggc acc ctg      175
381                               Met Ala Gly Thr Leu
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**VERIFICATION SUMMARY**

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